Supplemental Material

Suplemental Table

Table S1. Formation of Pks megacomplex as seen by fluorescence microscopy[a].

OD_{600}	Total Cell Count[b]	PksR-YFP Count	% PksR-YFP
0.66	185	17	9
1.06	357	33	9
1.39	283	49	17
1.44	277	57	19
1.66	326	173	49
1.84	459	385	81
3.17	594	415	68
4.07	183	119	63
5.26	600	368	61
6.46	367	157	43

[a]Fresh cells were washed once with PBS, resuspended in 20μM TMA, and observed in phase contrast, TMA and yfp, as described in Materials and Methods.

[b]Number of cells per microscopic field.

Suplemental Figures

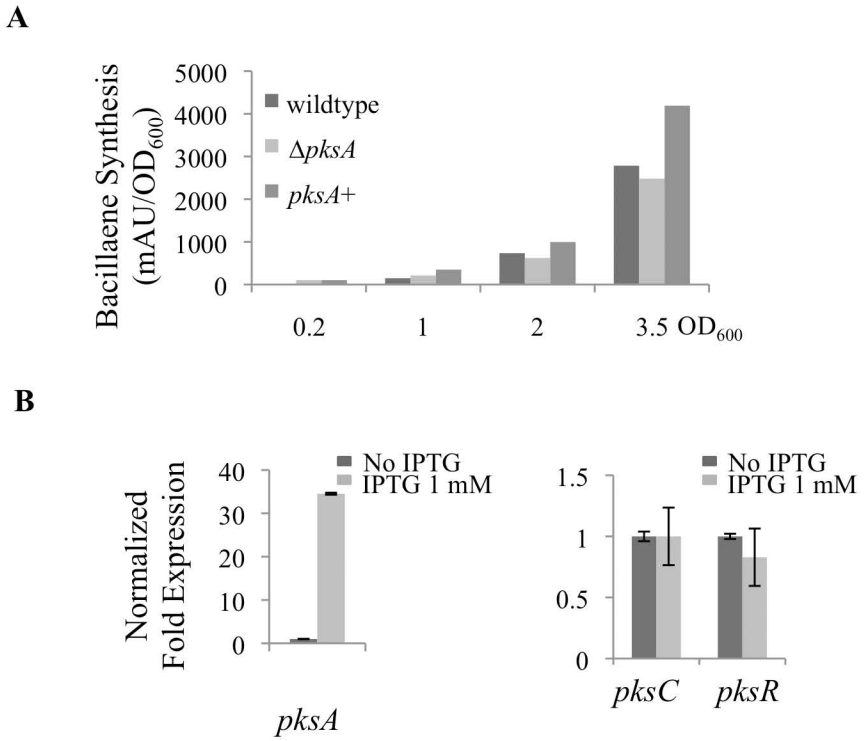

Figure S1. (A) Production of bacillaene over time in wild type, Δ*pksA* and *pksA*+. HPLC was performed as described in Materials and Methods. (B) qRT-PCR of *pksA, pksC* and *pksR* in a strain with PksA under the control of P_{hyper}. Similar conditions as described above were used to determine the mRNA abundance of *pksC* and *pksR* after overexpression of *pksA* with 1.0 mM IPTG. 35-fold overexpression of PksA was observed when culture cells where induced with IPTG. No fold changes in mRNA abundance of *pksC* and *pksR* were found.

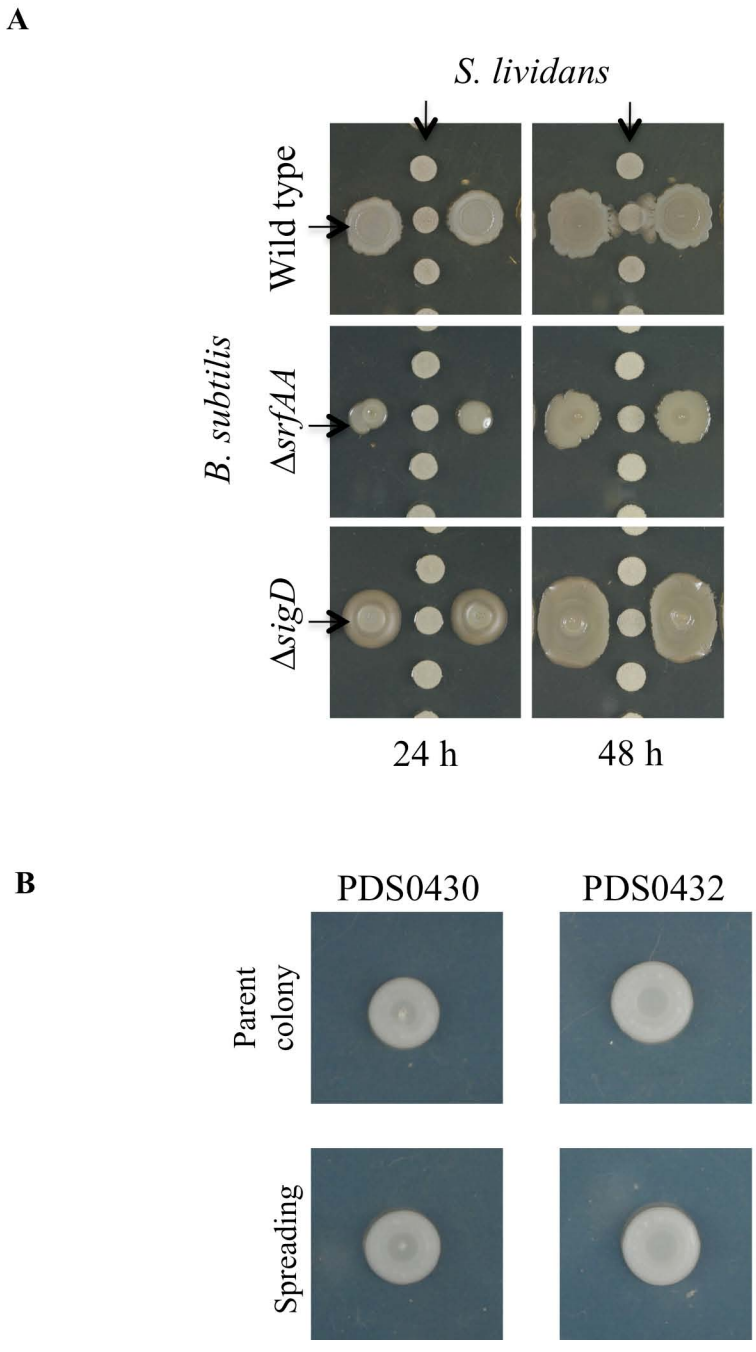

Figure S2. Spreading subpopulation resembles swarming motility (A) Co-culture of *S. lividans* and *B. subtilis* wild type, Δ*srfAA* and Δ*sigD* mutants. Conditions are similar to those described in Figure 2. *B. subtilis* mutants that lack *srfAA* or *sigD* genes were unable to spread towards *S. lividans* (B) Cells of PDS0430 (P_{hag}-YFP, P_{pksC}-YFP) and PDS0432 (P_{tapA}-YFP, P_{pksC}-YFP) were picked using a toothpick from the spreading subpopulations and plated on fresh agar medium in parallel with an inoculum from the original parent colony. No spreading occurred for either inoculation source and all colonies maintained the parent morphology in the absence of *S. lividans*.